Letters to the Editor

Phosphorylase kinase deficient liver glycogenosis: progression to cirrhosis in infancy associated with PHKG2 mutations (H144Y and L225R)

Editor—Deficiency of phosphorylase kinase (Phk), a regulatory protein kinase in glycogen metabolism, is the most frequent cause of hepatic glycogen storage disease (GSD). Patients typically present as infants with hepatomegaly, growth retardation, and raised triglycerides, cholesterol, and transaminases. Compared to other types of liver GSD, the condition is usually mild and its course is benign such that patients may even become asymptomatic as they grow up. Hypoglycaemia and lactic acidosis, for example, are uncommon in Phk deficiency in contrast to glucose-6-phosphatase deficiency (GSD type I). Hepatic architecture typically remains normal, unlike GSD III (debranching enzyme deficiency) in which hepatic fibrosis is common, and unlike GSD IV (branching enzyme deficiency) which usually progresses to cirrhosis in infancy. Only two infants with Phk deficiency and cirrhosis were found in five older Japanese patients, but it remains to be clarified whether this observation can be generalized and also applies to other ethnic groups.

Phk is a complex enzyme consisting of four different subunits, (αβγδ)₄, and isoforms or splice variants exist for each subunit. This gives rise to genetic and phenotypic heterogeneity of Phk deficiency. A muscle specific form of Phk deficiency is caused by mutations in the gene for the muscle subunit, PHKA1, which resides on the long arm of the X chromosome, whereas liver Phk deficiency can be caused by mutations in three genes: PHKA2, PHKB, and PHKG2. PHKA2 encodes the liver isoform of the α subunit. It is located on the short arm of the X chromosome and therefore involved in most (male) cases of liver Phk deficiency. PHKB, located on human chromo-
some 16, encodes the β subunit that is expressed in all tissues. PHKB mutations therefore cause autosomal recessive Phk deficiency of both liver and muscle, but liver symptoms predominate and the biochemical muscle involvement is often not clinically apparent. Ten different mutations in the PHKB gene have been identified in seven patients. PHKG2, also autosomal, encodes the testis/liver isoform of the catalytic γ subunit. PHKG2 mutations seem to be the rarest variant with only five patients described to date, all of them homozygous offspring of consanguineous parents.

A genotype-phenotype correlation is emerging in liver Phk deficiency. The functional impact of PHKB mutations, both on residual enzyme activity and clinical condition, appears to be mildest. In contrast, PHKG2 mutations seem to concentrate at the opposite end of the spectrum of severity with very low residual Phk activities, very high plasma lipids and transaminases, and other abnormalities that are uncommon in Phk deficiency, such as lactic acidosis, abnormal glucagon response, or hepatocellular adeno-

![Figure 1](http://jmg.bmj.com/figure.png)

Figure 1  PHKG2 missense mutations in a patient with Phk deficiency and liver cirrhosis. Sequencer tracings are shown on the left, with heterozygous mutation sequence references and alignment of additional protein kinase sequences.
was 1.6 U/g Hb (normal, 6-30) in erythrocytes and <1 U/g wet weight (normal, >20) in liver. Hepatic branching and debranching enzyme activities were normal. Liver histology showed fibrous expansion of portal tracts with portal-portal bridging and gross parenchymal glycogen deposition with minimal fat. Overnight nasogastric feeds and two-hourly daytime feeds were necessary to prevent hypoglycaemia and lactic acidosis. Firm irregular hepatomegaly and raised plasma transaminases persisted. Repeat liver biopsy at 3 years showed that glycogen deposition had diminished but cirrhosis was present, with broad bands of interportal fibrosis encircling parenchymal nodules.

Genomic DNA was purified from a blood sample and the PHKG2 gene amplified in four segments and analysed by direct sequencing in both directions, as described previously. The patient was found to be heterozygous for two single nucleotide replacements: a C to T transition replacing histidine 144 with tyrosine, and a T to G transversion replacing leucine 225 with arginine (fig 1). H144Y allele had been inherited from the father and the H144Y allele had been inherited from the mother, together accounting for the patient’s enzyme deficiency.

The patient described here is the first male case and the first to be found compound heterozygous for PHKG2 mutations, whereas all previous PHKG2 cases were female, homozygous offspring of consanguineous parents. All seven PHKG2 mutations identified to date in different subjects are unique. Including the patient described here, three liver Phk deficiency cases with early cirrhosis have now been analysed for mutations, and PHKG2 mutations were identified in all three. This suggests strongly that this rare complication of Phk deficient liver glycogenosis is generally caused by PHKG2 mutations. Among the first group of three other patients not selected for clinical severity in which PHKG2 mutations were identified, one had a mild course whereas two developed fibrosis but not cirrhosis at an early age together with other complications uncommon in Phk deficiency. A feature shared by all previous cases and the present one is a very low residual Phk activity and pronounced secondary biochemical abnormalities. Missense as well as truncating mutations are found among both the cirrhotic and the non-cirrhotic patients, so that no obvious correlation between mutation severity and cirrhosis is evident. Our observations suggest that patients with PHKG2 mutations have a much higher risk of severe liver disease than those with PHKA2 or PHKB mutations. The malignant potential of cirrhosis in this small subgroup is unknown.

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MANFRED K KILIMANN
Institut für Physiologische Chemie, Ruhr-Universität Bochum, D-44780
Bochum, Germany

†The Sheffield Children’s Hospital, University of Sheffield, Division of Child Health, Sheffield S10 2TH, UK

Correspondence to: Dr Kilimann, manfred.kilimann@ruhr-uni-bochum.de


Familial Wilms tumour resulting from WT1 mutation: intron polymorphism causing artefactual constitutional homozygosity

Editor—Familial Wilms tumour is rare, accounting for only 1-2% of cases, and is not usually associated with other tumour types or congenital malformation. The pattern of inheritance has been interpreted as a dominant predisposition to Wilms tumour with incomplete penetrance of approximately 30%. Following the isolation of the WT1 gene in 1990, it soon became clear that WT1 mutation did not account for any of the large Wilms tumour pedigrees and was found in only the minority (~10%) of sporadic Wilms tumours. Pedigree specific differences in age at onset, incidence of bilateral tumours, and presence of metastases provided further evidence for the existence of more than one gene for familial Wilms tumour. Recently, two familial Wilms tumour gene loci, designated FWTT and FWTT2, have been mapped by genetic linkage analysis to 17q12-21 and 19q respectively. While a series of Wilms tumour families were being analysed for linkage to the putative FWTT locus on 17q, one proband was noted to carry a tumour specific 11p13 deletion (the WT1 locus) and to suffer from genitourinary abnormalities (fig 1). Mutational analysis of WT1 was therefore undertaken in this pedigree.

Family WILMS 5 was identified as a sib pair affected with unilateral Wilms tumour. The sister (No 301) presented at the age of 2 years with a tumour of fetal rhabdomyomatous type and remains well 12 years later. Her brother (No 302) presented at the age of 4 years with a
tumour of biphasic histology (stromal and blastemal). He relapsed shortly after finishing standard treatment and subsequently died from progressive tumour. He suffered from severe bilateral cryptorchidism and hypospadias, and surgery showed the presence of persistent Mullerian structures as well as testicular tissue. His constitutional karyotype was 46,XY whereas metaphases from the tumour displayed an interstitial 11p13 deletion and an iso-chromosome 1q. Both parents were phenotypically normal with no history of Wilms tumour. There was no family history of other cancers or congenital malformation.

Sequencing of exon 7 of WT1, which codes for the first zinc finger, showed a heterozygous 7 bp deletion in constitutional DNA from both affected sibs. This frameshift is predicted to lead to the introduction of 59 novel amino acids following Ser318 with a termination codon before the zinc finger region, lead to the introduction of 59 novel amino acids following DNA from both a finger, showed a heterozygous 7 bp deletion in constitutional subsequently died from progressive tumour. He su...
change was common. Constitutional DNA from 16 normal people and two with Wilms tumours was sequenced, but none was found to carry the G to T change, implying that this base change is either a rare polymorphism or is specific to family WILMS. This illustrates the importance of verifying homozygous constitutional mutations using a second pair of PCR primers or an independent method.

This is only the fourth Wilms tumour pedigree where an inherited WT1 mutation has been identified. In the previously described pedigrees, one combined familial Wilms tumour with aniridia owing to transmission of a t(2;11)(q32;p13) with presumed complete deletion of the adjacent WT1 and PAX6 genes at 11p13. A father and son both had Wilms tumour associated with a constitutional 1 bp deletion in exon 6 of WT1, causing truncation of the protein before the zinc finger region. Only the son had urogenital abnormalities. In the third family, a nonsense mutation in zinc finger 2 was transmitted by an unaffected father to three daughters all affected by Wilms tumour. The same mutation has also been reported in a person with Denys-Drash syndrome but there were no features of this syndrome in this pedigree.

The mutation described in the pedigree in this report is novel, although mutations resulting in truncation of WT1 in exons 6 or 7, just before the zinc finger region, are described in sporadic Wilms tumours and in acute myeloid leukemia. In this pedigree, germline WT1 mutation was associated with severe genitourinary malformation in the male whereas the two females had normal development; the mother is clearly fertile and the daughter has gone through normal puberty. A similar sex difference in severity of genitourinary malformation is seen in patients with Denys-Drash syndrome, now that the syndrome has been expanded to include genotypic females with the characteristic nephropathy and Wilms tumour. This pedigree also shows the variable nature of tumour behaviour resulting from a common initiating event.

It has been suggested that there is a genotype-phenotype correlation in the histological appearance of Wilms tumours with WT1 mutations, with a predominance of differentiation into heterologous mesodermal derivatives, commonly muscle, cartilage, bone, or fat. Subject 301’s Wilms tumour did indeed show an extreme form of heterologous differentiation, towards muscle, with the fetal rhabdomyomatous subtype. However, her brother’s tumour had biphasic histology (strobal- and blastemal) with no heterologous differentiation. This difference may be because of the nature or timing of the second WT1 mutation during renal or tumour development. However, it is equally likely that different morphologies result from an identical initiating mutation owing to the inherent plasticity of renal development. This is clearly seen in Wilms tumours resulting from mutation in the FWT1 gene, where histologies range from classical triphasic Wilms to the fetal rhabdomyomatous subtype (Rahman and Pritchard-Jones, unpublished observations).

Germline WT1 mutations are also found in cases of Wilms tumour without a family history. The greatest number has been described in patients with DDS, but a few have been described in some patients with bilateral tumours or genitourinary abnormalities, particularly cryptorchidism, and in a small number of unilateral cases without congenital abnormalities. In a few of these cases, the mutation is inherited from an unaffected parent. Germline mutations causing truncations in exon 7 of WT1 have been described in four patients with sporadic Wilms tumour, all of whom had normal genitourinary development. This is in contrast with the severe abnormalities found in subject 302 and further indicates the extreme variability in phenotypic expression of WT1 mutations.

Given the excellent survival following treatment for Wilms tumour without the need for gonadotoxic chemotherapy, the rarity of familial WT1 mutation could be because of pleiotropic effects of germline WT1 on genitourinary development, causing reduced fertility in affected subjects. Constitutional WT1 mutations are more commonly found in certain congenital malformation syndromes predisposing to childhood genitourinary cancers (WAGR, Denys-Drash syndrome, and Frasier syndrome). Nevertheless, sporadic Wilms tumours occurring in conjunction with genitourinary abnormalities or showing heterologous differentiation can be the result of germline WT1 mutations. Screening of such patients and their relatives is advisable, particularly as unaffected subjects can carry mutations that might have severe consequences for their offspring. Ten of 21 patients with Wilms tumours showing heterologous differentiation had germline WT1 mutations. A recent report by the National Wilms Tumour Study Group found germline WT1 mutations in 7/28 Wilms tumour patients with cryptorchidism and 4/12 with hypospadias, but only 1/110 patients without genitourinary malformation. WT1 mutational screening can therefore probably be safely reserved for cases selected on the basis of associated abnormalities or tumour histology.

We thank Dr A M Potter, Centre for Human Genetics, Sheffield, for tumour cytogenetic data and Dr V Murday, St George’s Hospital, for culturing the skin fibroblasts. The skin fibroblasts from subject 201, RPK and RKL are supported by the Cancer Research Campaign and the Royal Marsden Children’s Cancer Unit Fund.

KATHY PRITCHARD-JONES* NAZNEEN RAHMAN† MARY GERRARD‡ DICK VARIEND§ LINDA KING-UNDERWOOD∥

*Section of Paediatric Oncology, Institute of Cancer Research, 15 Cotswold Road, Belmont, Sutton, Surrey SM2 5NG, UK
¶Section of Cancer Genetics, Institute of Cancer Research, Sutton, Surrey, UK
§Sheffield Children’s Hospital NHS Trust, Western Bank, Sheffield, S10 2TH, UK
∥Department of Histopathology, Sheffield Children’s Hospital NHS Trust, Sheffield, UK

Silver-Russell syndrome and ring chromosome 7

Editor—We read the recent paper by Miyoshi et al. with great interest. They report a child with Silver-Russell syndrome (SRS) and maternal uniparental disomy of chromosome 7 (mUPD7), with 30% mosaicism for an additional ring chromosome 7 of paternal origin. As the ring contained four CA repeat polymorphic markers which map to the region 7p13-q11 (D7S2552, D7S499, D7S494, and D7S2503), they concluded that imprinted genes within this region can be ruled out as candidates for SRS. While the data are interesting, we feel that they are inadequate to support this conclusion.

Firstly, the genetic distance spanned by the four markers used to define the extent of biparental inheritance is small (2.26 cM between 64.81 and 67.07 cM). Furthermore, UPD was shown using marker D7S506 which is estimated to lie less than 0.1 cM distal to D7S2552. The trisomic region is therefore likely to be considerably smaller than 7p13-q11. There are now more accurate localisations for at least two of the biparentally inherited markers; D7S499 and D7S494 have been mapped to 7p11.2 and 7p11.2-q11.1, respectively. The ring may therefore only include a small region close to the centromere, leaving 7p12-13 uninvolved. It is interesting to note that three genes (IGFBP1, IGFBP3, and GRB10), which have been proposed as candidates for SRS, lie between two markers (D7S2497 and D7S506) which are outside the potentially excluded region.

There is also no evidence to show that genes on the ring chromosome are active. Indeed, follow up of patients with supernumerary marker chromosomes has found that they are frequently not associated with any phenotypic effect. Finally, even if the ring chromosome is active, it can only be used to infer exclusion of a paternally expressed imprinted gene from the region. If the SRS gene is transcribed exclusively from the maternal allele, it will be overexpressed in this patient, whether or not the gene is located within the ring chromosome, since she has mUPD7.

In conclusion, caution should be used not to overinterpret the data reported by Miyoshi et al. Nevertheless, the findings do support the continuing search for a candidate imprinted gene(s) for SRS on chromosome 7. They also emphasise the importance of searching for cytogenetic abnormalities of chromosome 7 in SRS which will provide much needed clues to the region involved.

Emma L Wakeley*, Megan Hitchins**, Philip Stainer*, David Monk*, Gudrun E Moore*†, Michael A Preece*†

*Action Research Laboratory for the Molecular Biology of Fetal Development, Division of Paediatrics, Obstetrics and Gynaecology, Imperial College School of Medicine, Queen Charlotte’s and Chelsea Hospital, Goldhawk Road, London W6 0XG, UK
†Biochemistry, Endocrinology and Metabolism Unit, Institute of Child Health, University College London, 30 Guilford Street, London WC1N 1EH, UK

Correspondence to: Professor Preece, mpreece@ich.ucl.ac.uk

This letter was shown to Dr Miyoshi et al, who reply as follows.

Dr Wakeley et al suggest that the ring chromosome 7 observed in our SRS patient must be smaller than we estimated. This is based on databases: for example, the genetic distance between markers D7S506 and D7S2552 they cite is <0.1 cM. However, when using another database, it is calculated to be 1.1 cM. Since this discrepancy is obviously derived from the different databases used, and since not many DNA markers have physically been assigned to the chromosomal region, we tried to perform FISH mapping of D7S506, which is the most centromeric marker among those showing UPD(7)mat in our previous study, using a PAC clone (303F13) containing the marker as a probe. Consequently, the PAC was mapped to the 7p11.1-p11.2 region. This finding indicates that the four biparentally inherited markers (D7S2552, D7S499, D7S494, and D7S2503) we identified are located centromerically to D7S506 and the short arm breakpoint of the ring chromosome must lie between them. In addition, FISH analysis using a probe for the elastin gene locus (VYSIS, UK) that was localised to 7q11.23 gave no fluorescence signals on the ring chromosome. Therefore, the extent of the ring is smaller than the 7p11.2-q11.23 segment.

2 http://cedar.genetics.soton.ac.uk/pub/chrom7/map.html

Variants of STAT6 (signal transducer and activator of transcription 6) in atopic asthma

Editor—Atopy is characterised by raised IgE levels and it underlies the clinical disorder bronchial asthma. IL-4 and IL-13 play a key role in the development of asthma acting through the IL-4 receptor (IL-4R) and IL-13R, respectively. Since these two receptors share the IL-4Rα chain, this subunit is the crucial component required for IL-4 and IL-13 signalling. Recently, three coding variants in the human IL4R gene have been identified and these showed genetic and functional association with atopic asthma in different ethnic groups. The Ile50 variant was associated with atopic asthma in a Japanese population and Arg551 or Pro478 were associated with IgE levels in American and German populations, respectively, but perhaps through different mechanisms. Ile50 specifically and strongly upregulates cellular IgE synthesis through STAT6 when tested by cDNA transfection into human and murine B cell lines. Functional assay of

Arg551Gln IL-4Rα showed impaired binding of the negative regulatory molecule, protein tyrosine phosphatase, SHP-1, and increased expression of CD23 was found in peripheral blood mononuclear cells after challenge with human IL-4. 

However, this finding was not replicated by another group. 

In contrast, Pro478 is in tight linkage disequilibrium with Arg551 in a German population and may change the structure of the receptor, leading to altered phosphorylation patterns of signal molecules and hence lower IgE levels. 

The Stats are a family of transcription factors evolutionarily conserved from Drosophila to humans. 

The aim of this study was to test whether variants of the STAT6 gene relate to atopic asthma in both British (n=300) and Japanese (n=400) populations.

For the Japanese study, 100 adults from Osaka were randomly selected as controls from clients of a commercial medical examination company, with adjustment for the sex and age distribution of this area. 

We recruited 400 patients, 100 in each group, with atopic asthma, intrinsic (non-atopic) asthma, atopic rhinitis, and atopic eczema from Kawai Clinic, Wakayama Red Cross Medical Centre, and Habikino Hospital, respectively. We selected patients with one principal atopic clinical disorder at the time of examination.

For the British study, 150 subjects were randomly recruited from an obstetric outpatient clinic in Oxfordshire. One hundred and fifty subjects with physician-diagnosed atopic asthma were selected from the Oxford Chest Unit; both controls and patients were white.

All the asthmatic subjects had specialist physician-diagnosed asthma with (1) recurrent breathlessness and chest tightness requiring continuing treatment, (2) physician documented wheeze, and (3) documented labile airflow obstruction with variability in serial peak expiratory flow rates >30%. Marked asthma was designated as chronic rather than episodic asthma, needing chronic therapy with steroids. The diagnosis of rhinitis was based on chronic nasal obstruction or congestion, rhinorrhea, and sneezing, not caused by chronic infection. The diagnosis of atopic eczema was made on the basis of the morphological appearance of active skin disease, the distribution of skin lesions, the clinical course of the disorder, and a family history of atopy. All cases of eczema met the diagnostic criteria of Hanafin and Rajka. 

There were no heavy smokers (>20 cigarettes per day) among these subjects.

Specific IgE against 15 airborne antigens was detected by solid phase immunoassay, MAST (Hitachi, Tokyo, Japan), and we used previously described criteria for a positive titre. A high concentration of total serum IgE (Pharmacia CAP system, Uppsala, Sweden) was taken to be greater than the mean +2 SD, and defined as IgE responsiveness, was diagnosed as the presence of a high concentration of total serum IgE, a positive specific IgE titre (>0.35 kU/l) against one of 15 highly purified allergens, or a combination of these two features. 

DNA samples were extracted using a commercial kit (IsoQuick, Microprobe Corporation, Garden Grove, USA). cDNA was extracted using commercial kits (Pharmacia, Sweden). To detect variants, cDNA for the STAT6 coding region was amplified with primers 5’GAA GAC AGC AGA GGG GTT GC and 5’CGT TGG GGG TAGT AGA AGA G. 

Sequencing was conducted with the big-dye system (ABI, UK) and images were visualised in the commercialised POP-6 gel using the automated sequencer (ABI Prism 310 Genetic Analyser). Primers were 5’TGT CTC TGC CCC GTC TC or 5’GGT CCC CAC CTC AGC CAT G.15 

To conduct the genetic association study, PCR including 1.5 mmol/l of magnesium chloride and genomic DNA in a 30 µl mixture was performed in a Perkin Elmer Cetus thermal cycler. Primers were 5’GGG AAG TTC AGC CTC TGA GAC CC and 5’AGC TCT TGT GAC TCA G.14 

The unuffled sequence was exchanged to incorporate the restriction site. The amplification products were digested with AciI.

Contingency table analysis, odds ratios, 95% confidence intervals, and significance values were estimated by computerised exact methods (SPSS program version 8). Odds ratio (OR) was calculated between high and low risk genotypes and between high and low risk alleles. If the number in the column was less than 10, Fisher's exact test was used. Probability values from this test were corrected for multiple comparisons by multiplying the p value by the number of comparisons that were made (Bonferroni correction).

Mutation scanning enabled us to identify a G2964A variant in a 3’ untranslated region of STAT6. 

As shown in tables 1 and 2, the allele frequencies for STAT6 in the two control populations were quite different, p(G)=0.76, p(A)=0.24 in the British population and p(G)=0.33 and p(A)=0.67 in the Japanese population (χ²=82.2, df=2, p<0.000001). There was no significant association between atopic asthma and this STAT6 variant in the British population; no association was seen with any atopy or asthma phenotype. In the Japanese population, mild atopic asthma characterised by positive antigen specific IgE response (ASE) (<0.75 kU/l) or high total IgE (mean +2 SD) showed a strong association with this variant (OR=3.19 (95% CI: 1.40-7.08), p=0.0043, Pc=0.016).
Neither adult nor childhood asthma with a marked atopy phenotype (ASE > 3.5 kU/l and total IgE > mean + 2 SD) was associated with this variant of STAT6. Again, no atopy phenotypes were associated with this variant.

Recent genetic and functional studies highlight the importance of variants of IL-4Ra in the development of atopy; Ile50 upregulates cellular IgE synthesis and is associated with atopic asthma in a Japanese population, while Pro478 alters the binding affinity of IRS-1/2, and is associated with lower IgE levels. No association was found between atopic asthma and these variants in a British population. These findings emphasise the genetic heterogeneity of atopic disorders, even within one locus in different ethnic groups; they raise the question of interaction between variants of different components of the IL-4/IL-13 signalling pathway. BCL6 might repress stat6 activated transcription and a variant of BCL6 has been associated with marked atopy. Interactions among signal transduction molecules of IL-4Ra might explain the complex relationships between genetic variants and phenotypes in atopy and asthma.

The gene encoding human STAT6, spanning 19 kb on 12q13-14, consists of 23 exons. Genome wide searches for association with atopic asthma in a Japanese population, atopy; Ile50 upregulates cellular IgE synthesis and is associated with lower IgE levels. No association was found atopic asthma in Italian families.


Our present data, showing association between variants of STAT6 and asthma with mild atopy, support the candidacy of STAT6 as an “asthma” locus on 12q in a Japanese population. Also, the marked difference in genotype frequencies between the British and Japanese populations may explain the “genetic heterogeneity” among and within ethnic groups. Since G2964A variant is located in 3’UTR of the gene, the functional role of this variant remains unknown; it may be in linkage disequilibrium with so far unidentified but functional variants in the regulating or coding parts of STAT6 or variants of the immediately adjacent genes. Further studies are needed to clarify the role of the STAT6 variants in predisposing to asthma among different ethnic groups.

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No linkage or association of the IL-4Ra gene Q576R mutation with atopic asthma in Italian families

Editor—Atopy, a familial clinical syndrome of asthma, rhinitis, and eczema, is characterised by IgE mediated allergy, which results from genetic and environmental events. The disease is immunologically defined by the presence of specific IgE antibodies to common allergens and raised total serum IgE concentrations. Also, because of its high prevalence, age dependent penetrance, and assumed heterogeneity, the mode of inheritance is unknown. Several genes which affect IgE responsiveness have been reported.

Among the genes that have been reported to affect the atopic phenotype, that for IL4 regulates the production of IgE. Through its receptor (IL4-R), IL4 signals target cells and tissues to mount a response. The IL4-R α chain binds IL4 and mediates its effect through kinases attached to the intracellular domain. The IL4-Ra coding gene has been localised to the short arm of chromosome 16 (16p12.1). Sharing of maternal markers flanking the IL4-Ra gene was recently described, and it was reported to be associated with higher levels of expression of CD23 by IL-4, severe atopic dermatitis, raised serum IgE level, or a specific response to a common allergen in a case-control study with 20 affected and 30 unaffected adults in the North American population. This association study needs confirmation in a different sample.
In the present study we have investigated the frequency of the IL-4-Ra Q576R mutation in a large sample of Italian atopic asthmatic families to determine its involvement in genetic susceptibility to some atopic asthma related phenotypes.

A panel of 851 subjects was analysed, recruited from 192 families with one or more affected children, of whom 133 were attending the Allergy and Pulmonology Clinic of the Department of Paediatrics of the University of Verona, as described previously, and 59 families attending the Institute of Paediatrics of the Hospital in Bolzano, both located in north east Italy. All the subjects were tested for clinical history, total serum IgE level, skin prick test (SPT), and bronchial hyper-responsiveness (BHR). Clinical asthma was defined according to the American Thoracic Society criteria, including the response to a respiratory questionnaire. BHR to methacholine was defined as PC20<25 mg/ml. Atopy was defined by the presence of one or both of the following criteria: (1) positive SPT to one or more common aeroallergens, such as house dust mites, cat, dog, Alternaria, grass pollen, Parietaria; (2) raised circulating total IgE (from 0 to 10 years of age: age adjusted standard curve, levels above the 90th centile; after 10 years of age: 200 kU/l). Among the families, 522 atopic subjects, 477 with a positive SPT, 288 with raised total serum IgE levels, 298 with clinical asthma, and 281 with BHR were analysed. The total is greater than the total number of people, as two or more phenotypes could occur together in the same person.

Genomic DNA was extracted from whole blood, according to standard protocols. To achieve an easy and rapid evaluation of the guanine for adenine substitution at nucleotide 1902 of the IL4-Ra gene, a new protocol based on RG-PCR and nuclease digestion was developed. This method is faster than the single strand conformation polymorphism technique (SSCP) and DNA sequencing analysis previously described. A mutant oligonucleotide which inserted in the product of DNA amplification a new restriction site for DdeI was synthesised. The primers used were a novel 21-mer forward oligonucleotide (5'-TCGGCCGCGACCACTGGCCT-3') with an A1899C substitution, and the same reverse oligonucleotide previously described. The PCR product is a 298 bp fragment. Restriction analysis with DdeI results in two fragments of 277 and 21 bp for the Q576 allele, and a single fragment of 298 bp for the 576R allele, as shown in fig 1. All the subjects were genotyped. The data were analysed using the affected sib pairs method implemented in SIBPAL (SAGE package) and the transmission disequilibrium test. The frequency of the 576R mutation calculated in the family founders was 18% (PIC=0.25). In the normal controls, the allele R frequency was 17.5% (18/104 alleles). This frequency is 18% (PIC=0.25). In the normal controls, the allele R frequency was 17.5% (18/104 alleles). This frequency is greater than the total number of people, as two or more phenotypes could occur together in the same person.

Linkage analysis indicated no significant increase in allele sharing for atopy, SPT, IgE, BHR, or asthma, respectively. No allele transmission disequilibrium was observed. Association studies were performed with 52 adult unrelated controls in whom positivity for each of the phenotypes was excluded. Cases were collected from family founder members according to the phenotype (asthmatic: 45, BHR: 60, IgE: 71, SPT: 153, atopy: 175). The case-control analysis did not show a variation in the distribution of alleles between cases and controls in the phenotypes investigated. The statistical tests have sufficient power (80%) to detect an association with an odds ratio of 3 for IgE, SPT, atopy, and of 5 for asthma and BHR.

As the informativity of Q576R was limited (PIC 0.25), further linkage analyses with additional IL4-Ra polymorphisms may better define the putative involvement of the gene in hereditary susceptibility to atopic asthma. Wang et al have recently noted that mutation Q576R does not have a direct effect on IL-4 signal transduction in murine cells and suggested that the hyper-sensitive induction of CD23 in cells derived from human allergy patients may be the result of different or additional alterations in the IL-4 signalling pathway. Another IL4-Ra gene mutation, Ile50Val, was reported to be associated with atopic asthma, increased total IgE, and increased mite specific IgE in a Japanese population, and to upregulate B lymphocyte growth and IgE production in response to IL4 challenge. This mutation will now be investigated in the Italian group of patients.

The results reported in this paper were partially obtained by using the program package SAGE, which is supported by a US Public Health Service Resource grant (1 P41 RR03655) from the Division of Research Resources. This work was partially funded by Telethon Italy, Italian Ministry of University and Research, Italian CNR Target Project Biotechnology, and Consorzio Studi Universitari Verona and Italian CNR contribution N.99.02567. CT84 to FP3. The results reported in this paper were partially obtained by using the program package SAGE, which is supported by a US Public Health Service Resource grant (1 P41 RR03655) from the Division of Research Resources. This work was partially funded by Telethon Italy, Italian Ministry of University and Research, Italian CNR Target Project Biotechnology, and Consorzio Studi Universitari Verona and Italian CNR contribution N.99.02567. CT84 to FP3.

Important of the autosomal recessive retinitis pigmentosa locus on 1q31-q32.1 (RP12) and mutation analysis of the candidate gene RGS16 (RGS-r)

Editor—Retinitis pigmentosa (RP, MIM 268000) is the term applied to a clinically and genetically heterogeneous group of retinal degenerations primarily affecting the rod photoreceptors. RP is characterised by progressive loss of vision, initially manifesting as night blindness and reduction in the peripheral visual field, and later involving loss of central vision. Ophthalmoscopic examination typically shows pigmentary disturbances of the mid-peripheral retina. RP may be inherited as an autosomal recessive, autosomal dominant, digenic, or X linked trait. Autosomal recessive RP (ARRP) accounts for around 20% of all cases of RP, while sporadic RP, which is presumed to be recessive, accounts for around 50%. Mutations causing autosomal recessive RP (ARRP) have been found in the genes encoding rhodopsin, the α and β subunits of rod phosphodiesterase, the α subunit of the cyclic GMP gated channel protein, and the genes RPE65, RLBP1, ABCR, and TULP1. In addition, genetic linkage studies have identified ARRP loci at 1q31-q32.1, 2q31-q33, 6cen-q15, and 16p12.1-12.3. The initial set of markers chosen to be analysed were those known to flank the ARRP loci for which no gene corresponding to the loci of genes responsible for ARRP, as determined from the Généthon sex averaged genetic map. Primers were obtained from the MapPairs set (Research Genetics, Huntsville, AL), or synthesised commercially according to data from GDB (Johns Hopkins University: http:// gdbwww.gdb.org/).

Non-radioactive PCR was performed with 300 ng of genomic DNA, 10 pmol of each primer, 200 µmol/l dNTPs, 1.5 mmol/l MgCl₂, and 1 unit of Taq DNA polymerase. A three stage PCR consisting of 35 cycles of 94°C, 50-62°C, and 72°C, each for one minute, was used. The amplified products were then separated by electrophoresis on 6-8% non-denaturing polyacrylamide gels (Protogen, National Diagnostics) and stained with ethidium bromide. Two point lod scores were calculated using the LINKAGE package.

Primers for heteroduplex analysis and direct sequencing of the five exons and the intron-exon boundaries of the RGS16/RGS-r gene were designed using the published sequences.

Table 1 Known loci for ARRP including some of the polymorphic markers used in this study

<table>
<thead>
<tr>
<th>Gene</th>
<th>Reference</th>
<th>Markers used</th>
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<tr>
<td>RPE65</td>
<td>7</td>
<td>D1S1665, D1S1669</td>
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<tr>
<td>ABCR</td>
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<td>D1S256, D1S2813</td>
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<td>RP12</td>
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<td>D1S127, D1S128</td>
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<tr>
<td>1q31-q32.1</td>
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<td>D1S287, D1S292</td>
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Genomic sequence (Genbank AF009356) as follows: exon 1F - GCCTGCGCACCATCTGCGCCTAC; 1R - CTCTCTCTCAAGCCTCTAGC (208 bp); exon 2F - CACCACCCAGAGCTCCTCTGG; 2R - GTTGCCAAGGTCACCACTAGCG (312 bp); exon 3F - CAGCAATCACGACGGTGCTCTGG (281 bp); exon 4F - GATCCCCTAGTGTGCCAGCCTC; 4R CACCACCCAGAGCTCCTCTGG; 4R CACCACCCAGAGCTCCTCTGG; 4R CACCACCCAGAGCTCCTCTGG; 4R CACCACCCAGAGCTCCTCTGG.

Polymerase chain reaction PCR was performed in a 50 µl reaction with 1 µg of genomic DNA, 20 pmol of each primer, 200 µmol/l dNTPs, 0.75-1.5 mmol/l MgCl₂, and 1 unit of Taq DNA polymerase. A three stage PCR consisting of 40 cycles of 94°C, 55-60°C, and 72°C, each for one minute, was used. The resulting product was allowed to cool slowly to room temperature to maximise the formation of heteroduplexes.

All five exons of RGS16/RGS-r were directly sequenced in two or more members of each potentially 1q linked family using an automated sequencer (ABI Biosystems model 373). PCR products were purified and then reamplified using the FS kit (Perkin Elmer). Variants were sequenced in both the forward and reverse directions to confirm the location of sequence changes.

Acid restriction digests were performed directly on 20 µl of exon 4 PCR product by overnight incubation at 37°C. The resultant bands were photographed after electrophoresis on a 2% agarose gel and stained with ethidium bromide.

Three of the 14 families studied showed evidence of linkage to the 1q31-32.1 ARRP locus and were excluded by linkage analysis from all of the other ARRP loci (fig 1). Two of these pedigrees were of Pakistani origin (18RP and RP112) and one was Spanish (RP23/91). Analysis of additional polymorphic markers on 1q in these families did not permit further refinement of the RP12 locus.

Clinical examination of the small Spanish RP23/91 family showed para-arteriolar preservation of the retinal pigment epithelium (PPRPE) as previously described in RP12 linked families. A relative lack of pigmentation adjacent to retinal arterioles was also seen in the Pakistani RP112 family. This feature could not be conclusively shown in the 18RP pedigree, possibly because the three affected subjects are only 22, 14, and 13 years old respectively. The fundus photograph showing PPRPE in the

**Figure 1** Pedigrees of families exhibiting evidence of linkage to 1q31-32.1 showing haplotypes for polymorphic markers in this region. Maximum lod scores for each family were: 18RP Zmax=1.70 (at 0.00) for the marker F13B, RP112 Zmax=2.48 at D1S2622, and RP23/91 Zmax=1.63 at D1S408. The RP12 locus lies between markers D1S2757 and D1S2622. Black or hatched bars situated between the marker alleles indicate the affected haplotype.
that the phase of recovery from photodeactivation. In vitro experiments with purified Tu subunits have shown that the intrinsic GTPase activity of Tu is inadequate to account for the rapid hydrolysis of GTP that is observed in vivo.23 It has been postulated, therefore, that a GTPase activating protein (GAP) that is capable of greatly accelerating this process must exist in rod outer segments.

RGS16/RGS-r, which is highly expressed in the retina, has been proposed to fill the role of the Tu GAP.24 It has been shown in vitro that the rate of transducin GTPase activity in the presence of RGS16/RGS-r is sufficient to correlate with the in vivo recovery kinetics of the visual cascade, and that in addition RGS16/RGS-r facilitates signal termination by competing with and thereby displacing PDEγ from Tu.25 This biochemical evidence suggests an important role for RGS16/RGS-r in retinal photoreceptors.

Since the human gene for RGS16/RGS-r has been mapped to 1q25-1q31,26 and since in the present study it could not be excluded from the RP12 locus by analysis of the intron 3 polymorphism in the linked family PMK214, this gene must remain as a potential candidate for the ARRP linked to this locus. We failed to find any sequence changes in the coding region of the gene in our four families, though it is possible that disease causing mutations may lie in the promoter region of the gene, which was not screened.

This study must, however, reduce the prospect of RGS16/RGS-r mutations being found in other 1q linked families and lead to a renewed search for mutations within the RP12 critical interval.

We would like to thank the family members for taking part in this study. Drs David A R Bessant and Annette M Payne are supported by the Medical Research Council of the UK (grant No G0901094). We would also like to thank the Wellcome Trust for an Equipment Grant for the sequencing facility (No 039283/2/93/Z/MW/JF).

**References**

Incidence and molecular mechanism of aberrant splicing owing to a G→C splice acceptor site mutation causing Smith-Lemli-Opitz syndrome

EDITOR—Smith-Lemli-Opitz (SLO) syndrome (MIM 270400) is an autosomal recessive disorder characterised by a wide spectrum of developmental abnormalities including craniofacial malformations, growth and mental retardation, and multiple congenital anomalies.1–7 The disorder is caused by deficient activity of 7-dehydrocholesterol reductase (7-DHCR), the enzyme that catalyses the reduction of the C5=C6 (Δ7) double bond of 7-dehydrocholesterol to produce cholesterol.1–9 As a consequence, patients with SLO syndrome have low plasma cholesterol and raised plasma 7-dehydrocholesterol concentrations, thus constituting the biochemical hallmark used to confirm the clinical diagnosis of the syndrome. Recently, we and others have identified the cDNA coding for human 7-DHCR and confirmed that SLO syndrome is caused by mutations in the corresponding 7-DHCR gene.6,8 So far, 19 different disease causing mutations have been reported, which were identified after analysis of only 33 patient alleles. In our previous report, we described an aberrantly spliced mutant 7-DHCR cDNA with an insertion of 134 bp which we identified in two of three Dutch patients analysed with SLO syndrome, one of whom was a homozygote and the other a compound heterozygote.4 Upon translation, this insertion not only introduces additional amino acids but also causes a frameshift, which leads to an inactive, truncated protein with a changed C-terminus.4 Since the same insertion was also reported by two other groups,4,8 and since the affected patients were not related to one another, this finding suggested that the insertion is the result of a frequently occurring mutation. To evaluate this, we analysed 17 additional patients with SLO syndrome for the occurrence of the 134 bp insertion using allele specific RT-PCR. Furthermore, we studied the underlying mechanism that gives rise to the aberrant splicing, which results in the 134 bp insertion at the cDNA level.

First strand cDNA was synthesised from total RNA isolated from leucocytes or primary skin fibroblasts obtained from 17 patients who were diagnosed with SLO syndrome on the basis of clinical features and raised serum levels of 7-dehydrocholesterol. In the patients for whom fibroblasts were available, the biochemical defect was confirmed by the detection of reduced enzyme activity of 7-DHCR using a previously described ergosterol to brassicasterol conversion assay9 followed by sterol analysis using gas chromatography-mass spectrometry.10 To determine the presence of the 134 bp insertion, the first strand cDNA was used as template for the amplification by PCR of the second half of the coding region of 7-DHCR cDNA using primer set DHCRins113-95 [M13rev] and DHCR1563-1544 [M13rev] (table 1). This primer set generates a single fragment of 915 bp in control subjects and patients with SLO syndrome, who do not harbour the 134 bp insertion (fig 1, lanes 2 and 3). In the previously described patient who was a homozygote for the insertion,1 a single fragment of 1049 bp is amplified (fig 1, lane 4), while in a patient who is a compound heterozygote for the insertion, both fragments of 915 and 1049 bp are amplified. In compound heterozygotes, an additional intermediate sized fragment is frequently observed, which is a heteroduplex form composed of one strand of both fragments, as could be shown by mixing the 915 and 1049 bp fragments followed by one cycle of melting and annealing (not shown). Of the 20 patients thus analysed, including the three patients previously reported and three pairs of sibs, one patient was a homozygote and 13 patients heterozygotes for the insertion. Of these 14 patients, eight patients (including the homozygote and two pairs of sibs) were of Dutch origin, four patients of German origin (including one pair of sibs), one patient of Belgian and one patient of Spanish origin.

In their recent paper, Fitzky et al reported that two of their 13 patients with SLO syndrome were compound heterozygotes for the 134 bp insertion. They also indicated that the insertion was caused by a G→C transversion in the

<table>
<thead>
<tr>
<th>Primer*</th>
<th>PCR primers used in this study</th>
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<tbody>
<tr>
<td>DHCRins113-95 [M13rev]</td>
<td>TGGTACGCAACGTGCAAAGCAGCCGTCAGG</td>
</tr>
<tr>
<td>DHCR1563-1544 [M13rev]</td>
<td>GTCAAGCGGTCTTGCAGGCCG</td>
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PCR conditions are available on request. *Numbering of nucleotide residues according to previously published 7-DHCR cDNA sequence.9
splice acceptor site of intron 8 of the 7-DHCR gene, which is included in the 134 bp insertion of the corresponding cDNA, but they did not study the molecular background in further detail. Therefore, we amplified the corresponding DNA region by PCR from genomic DNA isolated from two control subjects and two patients with SLO syndrome to confirm that the insertion is caused by a mutation in a splice acceptor site and to determine the underlying mechanism that causes the specific splicing defect. To this end two separate primer sets were used. The first primer set consisted of a forward primer designed on the cDNA sequence 5' of the site of insertion (DHCR-ins 10–100) and a reverse primer designed on the 134 bp insertion sequence (DHCR-ins 113–139), which amplified a genomic DNA fragment of approximately 2 kb. The second set consisted of a forward primer designed on the 134 bp insertion sequence (DHCR-ins 113–139) and a reverse primer designed on the cDNA sequence 3' of the site of insertion (DHCR-ins 158–159), which amplified a genomic DNA fragment of approximately 120 bp. Taken together, these results indicated that the 134 bp insertion resulted from a partial retention of the 3' end of an intron with an approximate size of 2 kb.

Indeed, sequence analysis of the two overlapping genomic DNA fragments which were amplified from the two control subjects identified consensus sequences for both a splice donor site and a splice acceptor site, which confirmed that the complete intron sequence, which comprises 1965 bp, was isolated (fig 2). Sequence analysis of the same overlapping genomic DNA fragments amplified from the two patients with SLO syndrome confirmed that the retention was caused by a G→C transversion at the −1 position of the splice acceptor site of the intron. This mutation disrupts the consensus sequence of the splice acceptor site and leads to alternative splicing of the transcript at a site located 134 bp 5' of the original splice site. The intron DNA sequence adjacent to this alternative site of splicing shows strong homology to the consensus sequence of a splice acceptor site and is preceded by a DNA sequence which has strong homology to the branch point consensus sequence, thus constituting quite a strong alternative splice acceptor site (fig 2).

The (compound) heterozygous presence of the 134 bp insertion enabled allele specific amplification by PCR of the two cDNAs, which could then be directly sequenced to identify the syndrome causing mutations on both alleles. To amplify the cDNA without insertion, primers DHCR-ins 960 and DHCR-ins 979, which both span the site of insertion (after nucleotide 963), were used in combination with, respectively, a forward primer in the 5' (DHCR-ins 113) and a reverse primer in the 3' region (DHCR-ins 158–159). This amplification produced two overlapping fragments of 1073 and 650 bp, respectively (fig 3). The cDNA containing the 134 bp insertion was specifically amplified using the same 5' and 3' region primers in combination with the DHCR-ins 113–157 and DHCR-ins 960–158 primers designed on the insertion DNA sequence. This amplification produced two overlapping fragments of 1170 and 748 bp, respectively (fig 3). Using the latter two primer sets, the cDNAs containing the 134 bp insertion which were identified in the patients with SLO syndrome (see above) were amplified and analysed by sequencing. In all cases, the same G→C mutation at the −1 position of the splice acceptor site was identified.

To conclude, using allele specific 7-DHCR cDNA amplification, we analysed 20 patients with SLO syndrome and identified one patient as a homozygote and 13 patients, including three pairs of sibs, as heterozygotes for the G→C mutation.
transversion which results in the partial retention of intron 8 owing to alternative splicing. After excluding the three sibs, this amounts to an incidence of ∼35% (12/34 alleles) for the mutant allele in our group of patients. When patients previously reported by others are also included, however, the incidence of this allele approximates ∼25% (15/59 alleles). This makes this allele the most frequently occurring among SLO patients, since all other causative mutations identified to date have been recurrent among a limited number of patients (unpublished results). The RT-PCR based methods presented in this paper provide an easy and rapid screening at the cDNA level for this allele specific amplification of cDNAs in case of heterozygosity for the 134 bp insertion allows the establishment of compound heterozygosity without subcloning of the cDNAs, which is valuable in cases where no parental material is available.

The relatively high incidence of the splice acceptor site mutation among patients with SLO syndrome makes this allele the most frequently occurring mutant allele. The allele specific amplification at the cDNA level for this mutation identified in our group of patients. When patients previously reported by others are also included, however, the incidence of this allele approximates ∼25% (15/59 alleles). This makes this allele the most frequently occurring among SLO patients, since all other causative mutations identified to date have been recurrent among a limited number of patients (unpublished results). The RT-PCR based methods presented in this paper provide an easy and rapid screening at the cDNA level for this allele specific amplification of cDNAs in case of heterozygosity for the 134 bp insertion allows the establishment of compound heterozygosity without subcloning of the cDNAs, which is valuable in cases where no parental material is available.

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Clinical and molecular cytogenetic studies of a large de novo interstitial deletion 16q11.2-16q21 including the putative transcription factor gene SALL1

Editor—Interstitial deletions of the long arm of chromosome 16 share common clinical features including growth retardation, failure to thrive, microcephaly, high and prominent forehead, prominent metopic suture, large anterior fontanelle, hypertelorism, broad nasal bridge, low set and dysplastic ears, cleft palate, micrognathia, short neck, narrow thorax, broad first toes, mental retardation, muscular hypotonia, congenital heart defects, and gastrointestinal as well as renal anomalies. More than 26 patients with different interstitial long arm deletions of chromosome 16 have been reported. Recently, mutations in the transcription factor gene SALL1 on chromosome 16q12.1 were shown to result in Townes-Brocks syndrome, an autosomal dominantly inherited malformation syndrome characterised by malformations of the anus, hands, and ears as well as deafness. We describe a fetus with the 16q deletion syndrome and additional features, including unilateral radial aplasia, ulnar hypoplasia, preaxial hexadactyly, and segmentation defects of the vertebral column. Some of these features overlapped with the malformations seen in Townes-Brocks syndrome. We therefore investigated the hypothesis that the SALL1 gene was included within the deletion.

The 31 year old, gravida 2, para 1 (her first child is a healthy boy) was referred at 24 weeks gestation because her fetus had cleft lip and palate detected by ultrasound screening. Biometry showed asymmetrical growth retardation with a thoraco-abdominal diameter of 43 mm (<5th centile) corresponding to 19 weeks’ gestation, while the BPD (60 mm) and femur length (41 mm) were within normal limits. Careful examination by ultrasound showed multiple fetal abnormalities. Dilatation of the lateral ventricles, a dilated third ventricle, and a cavum septum pellucidum were noted. Aplasia of the right radius was

Figure 3 Allele specific amplification of cDNAs with and without the 134 bp insertion. The 7-DHCR cDNA without the 134 bp insertion was specifically amplified in two overlapping fragments from a patient heterozygous for the insertion (lanes 2 and 3) and a patient with two missense mutations (lanes 6 and 7) using primer sets DHCR<sub>ins</sub> and DHCR<sub>−</sub> (lanes 2 and 6), and DHCR<sub>ins</sub> and DHCR<sub>−</sub> (lanes 3 and 7), respectively. The cDNA containing the 134 bp insertion was specifically amplified in two overlapping fragments from the heterozygous patient using primer sets DHCR<sub>ins</sub> and DHCR<sub>−</sub> (lane 4), and DHCR<sub>ins</sub> and DHCR<sub>−</sub> (lane 5). Using the latter two primer sets, no fragments were amplified from the patient who had two missense mutations and lacked the splice site mutation causing the insertion (lanes 8 and 9).

transversion which results in the partial retention of intron 8 owing to alternative splicing. After excluding the three sibs, this amounts to an incidence of ∼35% (12/34 alleles) for the mutant allele in our group of patients. When patients previously reported by others are also included, however, the incidence of this allele approximates ∼25% (15/59 alleles). This makes this allele the most frequently occurring among SLO patients, since all other causative mutations identified to date have been recurrent among a limited number of patients (unpublished results). The RT-PCR based methods presented in this paper provide an easy and rapid screening at the cDNA level for this allele specific amplification of cDNAs in case of heterozygosity for the 134 bp insertion allows the establishment of compound heterozygosity without subcloning of the cDNAs, which is valuable in cases where no parental material is available.

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suspected. The left kidney was absent. The right kidney was supplied by two arteries. The heart showed tetralogy of Fallot with absent pulmonary valve, agenesis of the ductus arteriosus, and a right sided aortic arch. The lungs were hypoplastic. Amniotic fluid, placenta, and umbilical vessels were normal. A fetal blood sample was taken for chromosome analysis. Necropsy examination after the parents opted for termination of the pregnancy in the 25th week of gestation showed a male fetus 31 cm in length and 690 g in weight (corresponding to the 24th/25th week of gestation). The fetus had a large neurocranium. Facial features included a prominent nasal bridge, a broad nose, hypertelorism, and upward slanting palpebral fissures. The ears were dysplastic, small, and deeply set with a single, left sided preauricular tag. The fetus had left sided cleft lip and palate. The chest was narrow. There was anal stenosis. In the upper extremities, the right radius was absent, while the ulna and thumb were hypoplastic. The left hand displayed preaxial hexadactyly with a finger-like thumb. Crowding of the toes was seen on both feet (figs 1 and 2).

X-rays confirmed the right radial aplasia and a shortened and thickened ulna. There was a single ossification centre (1 mm in diameter) within the hypoplastic right thumb, and a single ossification centre (1 mm in diameter) within the additional left thumb. The distal ossification centre of the additional left thumb was missing. The spine showed multiple segmentation defects (fusion of the third and fourth thoracic vertebral bodies, malformation of the eighth thoracic vertebral body, and aplasia of the third to fifth sacral vertebral bodies). Examination of the heart disclosed a perimembranous ventricular septal defect (4 mm in diameter), aplasia of the semilunar pulmonary valve, agenesis of the ductus arteriosus, and overriding of the right descending aorta. The left kidney was absent.

Chromosome analysis of fetal lymphocytes showed a large interstitial deletion of the long arm of chromosome 16 in all metaphases analysed. The result was confirmed by chromosome analysis of fetal fibroblasts. The karyotypes of the parents were normal. To define the exact site of the deletion, comparative genomic hybridisation (CGH) and fluorescence in situ hybridisation (FISH) analysis were performed. CGH was performed with fetal DNA as described elsewhere. CGH analysis defined the deletion to encompass bands 16q11.2 to 16q21 (fig 3). FISH analysis was performed using YACs from within and outside the deletion. YACs 922f01 (D16S415), 965g04 (D16S514/ D16S739), and 957h03 (D16S400/D16S3129) residing in 16q12-16q21 were shown to give only one signal on the normal chromosome 16, but none from the deleted chromosome 16. The STS numbers mapped to the corresponding YAC clones are given in parentheses. YAC 821g09 (D13S3021) located in 16q22 was not deleted. In addition, FISH using a PAC clone (reference: LLNL70403126Q4) including the SALL1 gene showed heterozygous deletion of SALL1 (fig 4). DAPI banding confirmed the loss of the whole heterochromatin of chromosome 16 harbouring the deletion. The resulting fetal karyotype was defined as 46,XY,del(16)(q11.2;q21) according to ISCN.

The phenotype of the 16q deletion syndrome was attributed to the deletion of critical bands at 16q11.2-q13, 16q21, 16q22.1. Specific features, such as congenital cataract and iris coloboma, result from more distal deletions of 16q22.3 and 16q23.1-24.2. Some of the features documented in patients with proximal deletions of chromosome 16q are also seen in Townes-Brocks syndrome. The clinical presentation of TBS is highly
kidneys. Twins with a deletion of 16q12.2−13 showed proximally placed thumbs, and bilateral, symmetrically small included dysplastic ears with abnormal folding of the helices, deletion of 16q12.1. Features described in these sisters reported.41 42 SALL1 SALL1. The cardiac defects might also result from the observed in the fetus result from heterozygous deletion of ear anomalies, hand anomalies (preaxial polydactyly, hypoplastic thumbs), abnormalities of the feet (syndactyly, club foot), deformities of the outer ear ("lop ears") and preauricular tags, and deafness.38 Renal malformations include agenesis as well as hypoplastic or polycystic kidneys and may lead to renal failure.39 The frequency of cardiac defects in TBS is high in those patients evaluated for cardiac defects by echocardiography.40 Mental retardation has rarely been reported.41 42 TBS is caused by mutations of the SALL1 putative transcription factor gene located on chromosome 16q12.1.18 All mutations so far identified in TBS patients are predicted to result in a prematurely terminated SALL1 protein lacking all double zinc finger domains thought to be essential for SALL1 gene function. Therefore, TBS is strongly suspected to result from haploinsufficiency for SALL1. This hypothesis is strengthened by the observation of a chromosomal translocation and a pericentric inversion in TBS patients, both involving a common breakpoint at 16q12.1.19 43 The features of the fetus reported here show overlap with TBS. Our FISH studies prove that one allele of SALL1 is indeed deleted. Therefore, we suggest that the ear anomalies, hand anomalies (preaxial polydactyly, hypoplastic thumb), anal stenosis, and the renal agenesis observed in the fetus result from heterozygous deletion of SALL1. The cardiac defects might also result from the SALL1 deletion, since two TBS patients with tetralogy of Fallot have been described previously.15 16 The anomalies of the radius and ulna seen in the fetus most likely result from the deletion of a contiguous gene in the deleted region. Vertebral segmentation defects have only recently been reported in a TBS patient.41 However, a SALL1 mutation has not been found in these patients.

Hoo et al42 presented two mentally retarded sisters with a deletion of 16q12.1. Features described in these sisters included dysplastic ears with abnormal folding of the helices, proximally placed thumbs, and bilateral, symmetrically small kidneys. Twins with a deletion of 16q12.2−13 showed ectopic anus, congenital heart defects, and dysplastic ears.12 A 10 year old boy with a de novo interstitial deletion 16q12.1q13 presented with micrognathia, a median cleft, low set dysplastic ears, a preauricular appendage, fusion of the third and fourth and the fifth and sixth vertebrae of the neck, hypospadias, hydrocephalus, sensorineural hearing deficits, and additional dysmorphic features.13 Further clinical features described in patients with deletions of the proximal long arm of chromosome 16 are summarised in table 1. Whether or not SALL1 is deleted in those patients reported with features similar to TBS and with deletions including 16q13 but not 16q12.1 remains to be elucidated.11 12 Some families have been reported in which affected subjects show features typical of both TBS and Goldenhar syndrome/oculoauriculovertebral spectrum.48 49 One family was described with hemifacial microsomia and radial ray defects.40 The affected members of this family displayed abnormal ears, multiple preauricular tags and pits, and unilateral micrognathia. In addition, triphalangeal thumbs, unilateral preaxial polydactyly, and a slightly anteriorly placed anus were present. Autosomal dominant inheritance was suggested in this family. Unilateral microphthalmia and facial asymmetry were observed in a family with anteriorly placed anus, irregular toes, and a digitalised thumb.50 Gabrielli et al48 described an infant with facial asymmetry, abnormal ears, preauricular tags, and anteriorly placed anus without triphalangeal thumbs or vertebral anomalies. Recently, a SALL1 mutation was detected in the patient described by Gabrielli et al48 showing that SALL1 mutations can also result in a Goldenhar-like phenotype.33 It remains to be seen if the affected subjects in the families reported by Johnson et al48 and Moeschler et al50 also carry mutations in SALL1.

In summary, our results suggest that haploinsufficiency for SALL1 might contribute to TBS-like features seen in the fetus presented here. In addition, certain clinical features in patients with proximal deletions of 16q including q12.1 are likely to result from haploid SALL1 deletions. Nevertheless, the interstitial deletion in this fetus probably includes several hundred genes, arguing against a simplistic additive genetic model to explain the observed phenotype. Moreover, additional features of the 16q deletion syndrome, which are not part of the phenotypic spectrum of TBS, are likely to be caused by the deletion of additional genes located within the deletion. Some clinical features might be non-specific and cannot be attributed to the deletion of a single gene. FISH studies should indicate whether SALL1 is deleted in those patients reported with features similar to TBS but with deletions including 16q13 but not 16q12.1. If a SALL1 deletion cannot be confirmed in these patients, a TBS-like phenotype in these patients might still result from a position effect influencing SALL1 gene expression.

Table 1 Clinical characteristics of patients with a deletion of the long arm of chromosome 16 including 16q12.1 or 16q13

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<td>T T</td>
<td>Small</td>
<td>SC</td>
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<tr>
<td>Malposition of toes</td>
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<td>+</td>
<td>+</td>
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<td>+</td>
</tr>
</tbody>
</table>

SN = sensorineural deafness; polydact = preaxial polydactyly; T = proximally placed thumbs; SC = simian creases.

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Reference address for YACs: http://www.mpimg-berlin-dahlem.mpg.de; http://www.mpimg-berlin-dahlem.mpg.de/~cyogen/CHRM16.HTM. We would like to thank Karin Lehmann and Gundula Lescich for expert technical assistance. Dr Friedrich C. Luft beta us with the text. This work was funded in part by a grant from the Wilhelm-Sander-Stiftung to JK.
Oculocutaneous albinism type 2 with a gene missense mutation in a patient with Angelman syndrome

Editor—Oculocutaneous albinism type 2 (OCA2) is an autosomal recessive disorder characterised by defective melanin production of the skin, hair, and eyes,1 which is also well established that AS and PWS deletion patients usually are hemizygous for the imprinted alleles of two PWS plus OCA2 patients who had a paternally inherited deletion of 15q11-q13.23 Here we reported previously.8 Physical examination showed the

11 The overexpression of SALL1 gene is located in 15q11-q13, which is deleted in the majority of patients with Angelman syndrome (AS) and Prader-Willi syndrome (PWS). The P gene is not imprinted and both alleles are expressed. PWS and AS patients with typical deletions are thus hemizygous for P. It is also well established that AS and PWS deletion patients usu-

show hypopigmentation of the skin and hair, and P is suggested to be responsible for this hypopigmentation as well,2 although the mechanism has not yet been established. A small intragenic deletion and a V443I missense mutation of the P gene were identified in the maternally inherited alleles of two PWS plus OCA2 patients who had a paternally inherited deletion of 15q11-q13.3 Here we describe the first evidence that a P gene mutation is responsible for OCA2 associated with AS.

The male patient was born at 38 weeks’ gestation to unrelated Japanese parents. There were no complications of pregnancy or delivery, but the birth weight, 1850 g, was small for gestational dates. Generalised albinism was noted at birth. Motor development was delayed, and he had a generalised tonic-clonic convolution at the age of 18 months. He was admitted to hospital at the age of 19 months because of non-convulsive epileptic status, as reported previously.4 Physical examination showed the

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typical facies of AS, including prominent mandible, protruding tongue, and relatively small head circumference (−1.72 SD). His skin and hair pigmentation was markedly reduced consistent with albinism (fig 1A). His hair colour was fair-blonde. Ophthalmological examination showed reduced pigmentation of the iris and a tigroid appearance of the retina with mildly reduced pigmentation. There was no nystagmus or other visual problems. He began walking unassisted at the age of 9 years with an ataxic gait typical of AS with the “hands up” position. He had severe mental retardation and could not speak. His skin, hair, and eye pigmentation gradually increased and he had dark hair by 12 years of age (fig 1B). His father and brother showed mild hypopigmentation of the skin and hair compared with other family members.

High resolution chromosome analysis and fluorescence in situ hybridisation (FISH) using D15S10 (Vysis, Downers Grove, Illinois) as probe showed a karyotype 46,XY,del(15)(q11q13) in the patient. Parental origin of the deletion was studied by the DNA methylation test using SNRPN exon 1 as probe.9 Genomic DNA was extracted from the patient and parents by a standard procedure.9 The SNRPN DNA methylation test indicated that the patient had only a paternal methylation pattern, indicating a maternal origin of the deletion (data not shown). These molecular cytogenetic results confirmed the clinical diagnosis of AS.

To screen for a P gene mutation, all 25 exons and flanking introns of the P gene were amplified by polymerase chain reaction (PCR) using the primers described by Lee et al.4 Agarose gel purified with GFX PCR and Gel Band Purification Kit (Amersham Pharmacia Biotech, Uppsala, Sweden), and direct sequenced with the ABI PRISM BigDye Terminator Cycle Sequencing Ready Reaction Kit. Sequence reactions were run on a Perkin-Elmer 310 Automatic Sequencer and analysed by use of LASERGENE software (DNASTAR, Madison, WI). A missense mutation A481T (1441G>A) as well as non-pathological polymorphisms (IVS11-4A>G, G780G (2340C>T), S788S (2364G>A)) of the P gene were identified in the patient (fig 2). The 1441G>A mutation is located in exon 14 of P and causes amino acid substitution of alanine for threonine at codon 481. The non-pathological polymorphisms have been previously described in other people.4 No wild type sequence was identified at these positions in the patient, as expected with hemizygosity at this locus. The father was shown to be heterozygous for the A481T mutation, whereas the mother was homozygous for the wild type allele (fig 2).

In this study the AS patient with OCA2 was shown to have a typical large deletion on the maternally inherited chromosome 15q, and a missense P mutation (A481T) on the paternally inherited chromosome. Most AS and PWS deletions are of similar size and P is always deleted in these patients.5 Since the patient has only the A481T mutation allele, the mother is homozygous for the normal allele, and the father is heterozygous for the A481T mutation allele and the normal allele, the maternally inherited P allele must be deleted in the patient. This was confirmed for the deletion origin by methylation analysis with the adjacent imprinted region of 15q11-q13.

AS patients with the common 15q deletion are frequently associated with hypopigmentation, whereas other classes of AS patients are less often hypopigmented.10 11
Anticipation in progressive diaphyseal dysplasia

EDITOR—Progressive diaphyseal dysplasia (MIM 131300) is an autosomal dominant osteochondrodysplasia with late onset and marked variability in expression of clinical and radiological features.1 We have recently described a patient with this diagnosis and suggested the presence of anticipation,2 the tendency of a familial disorder to occur earlier in the younger than in the older generations of a family.3

In order to assess whether this hypothesis was true, we examined 24 other people from the same family (fig 1) who were invited and agreed to participate. We excluded the proband and tried to avoid ascertainment bias by including in the study all family members who were alive in four generations. Although the diagnosis of progressive diaphyseal dysplasia had not been previously recorded in any of them, some family members had assigned to themselves the status of affected or unaffected. This was often discordant with the clinical and radiological data. It is also likely that people with bone complaints were more eager to consent to medical observation.

All family members were personally examined. The presence or absence and the age of onset of pain in the limbs, easy fatiguability, headache, poor appetite, and difficulty in running were recorded. Height, weight, and OFC were determined. Skull, spine, and limb morphology was examined and exophthalmos, muscle mass and strength, joint movement, tendon reflexes, and walking were assessed. Bone radiographic surveys, haemoglobin, white blood cell count, erythrocyte sedimentation rate, and serum alkaline phosphatase were performed.

The diagnosis of progressive diaphyseal dysplasia was clinically and radiologically established in 15 family members of the proband (table 1). Five of these have been previously described.2
We were able to determine the age of onset of the disease in these 15 patients (table 1), five from generation III and 10 from generation IV. Age of onset of the disease was defined as that of the initial symptom. The earlier age of the younger generation in the younger generation was statistically significant (table 2). A similar analysis applying the same criteria to the data previously described in another extended family with progressive diaphyseal dysplasia5 gave identical results (table 2). Our published pedigrees do not describe large families and often do not mention the age of onset of the disease.5–10 However, the available data, excluding once again the probands, is in accordance with the previous results (table 2).

A previous suggestion that anticipation was enhanced in father to son transmission1 is not supported by these new data; the patient with the earliest age of onset and one of the most severely affected is a female (IV.12, fig 1, table 1), who inherited the disease from her mother.

As has been previously pointed out, statistical anticipation without biological anticipation would occur if the disorder reduces fertility.7 However, the mean number of children in the family members of generation III is 2 for those that are healthy and 2.8 for those that are affected. The small number of people of generation IV who have already had children does not merit consideration.

Another type of bias could be that some of the younger persons might be classed as unaffected but might develop the disease later. This would inevitably increase the mean age of onset as assessed in the younger generation. However, the reported ages of onset of progressive diaphyseal dysplasia are between 4 and 32 years and in 25 patients all but four had ages of onset younger than 20, the exceptions being the ages of 21, 25, 30, and 32 years old.8,9 In order to avoid this bias, we did not include the data on three persons, one of whom is affected, from generation V. The ages of the unaffected persons from generation IV are 16, 23, and 24 years.

Although anticipation was only accepted as a true biological concept in the last decade, the list of conditions exhibiting it is growing rapidly.10 Most of them are neuropsychiatric diseases and trinucleotide repeat expansions are usually suggested to be the cause. This report suggests that anticipation occurs in progressive diaphyseal dysplasia and widens the disease spectrum of this concept to bone dysplasias. A dynamic mutation with trinucleotide repeat expansion may or may not be the cause of this osteochondrodysplasia of dense bone with unknown pathogenesis. The search for the molecular explanation of this and other rare genetic disorders that cause dense bones could disclose approaches to more common health problems such as osteoporosis.12

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JORGE M SARAIVA
Consulta de Genética, Hospital Pediátrico de Coimbra, and Servicio de Genética Médica, Faculdade de Medicina de Coimbra, Avenda Bissaya-Barreto, 3000 Coimbra, Portugal. Jpsgw@hotmail.com

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Hereditary neuropathy with liability to pressure palsies: two cases with a reciprocal translocation t(16;17)(q12;p11.2) interrupting the PMP22 gene

Editor—Hereditary neuropathy with liability to pressure palsies (HNPP) or tomaculous neuropathy is an autosomal dominant disease. HNPP patients present with acute or recurrent transient muscle palsies and paraesthesias, usually after minor trauma. HNPP is characterized from the pathological point of view by the presence of sausage shaped swelling of the myelin sheath or tomacula in sensory and motor nerves.

A deletion on the proximal short arm of chromosome 17 was detected in affected members of HNPP families. The deleted region is the same as that duplicated in Charcot-Marie-Tooth disease type 1 (CMT1A). While the CMT1A phenotype is mostly the result of extra dosage of the genes contained in this duplicated region, the HNPP phenotype results from monosomy of the same region in over 85% of cases. This duplication/deletion event is thought to occur because of the unequal crossing over between two large repeats bordering the CMT1A region, which encompasses 1.5 Mb of 17p11.2.

The association between CMT1A and the peripheral myelin protein 22 (PMP22) gene, located within the CMT1A duplicated region, was established by the finding of point mutations in this gene in CMT1A patients. The PMP22 gene spans approximately 40 kb and contains four coding and two 5′ untranslated (1A and 1B) exons. In unrelated patients with inherited peripheral neuropathies, 27 mutations in the PMP22 gene have been described, affecting the different domains of the protein, some of them leading to a truncated protein. The clinical phenotypes of the patients carrying mutations in the PMP22 gene are variable, giving some clues about correlations between phenotype and genotype. Five mutations in the PMP22 gene have been described that result in a HNPP phenotype: two frameshift mutations, two non-sense mutations, and a splice site mutation.

We report here a pedigree with two affected members (mother and son) with HNPP, both of whom carry a reciprocal translocation t(16;17)(q12;p11.2), which we have studied by FISH. The breakpoint on chromosome 17 in both patients lies within exons 1a to 3 of the PMP22 gene.

The proband is a 24 year old male referred to our clinic for molecular analysis to confirm the clinical diagnosis of HNPP. The mother confirmed delayed milestones during infancy, followed by clumsiness and difficulties with running and schooling during childhood and adolescence. At the age of 21, he had two episodes of numbness and muscular weakness of the left arm following compression while sleeping and weight lifting, without full recovery. Clinical examination showed distal muscle atrophy and weakness of the left arm involving the long distal extensors of the upper limb, the abductor of the thumb, and the supinator of the arm. He was able to walk on his toes and heels and had normal reflexes. No other signs of muscle weakness were noted. Nerve conduction studies showed delayed and reduced sensory action potentials with prolonged motor latencies and slow motor conduction velocities (table 1). Clinical and electroneurographic studies were also carried out in the parents and his twin sister. The mother was clinically asymptomatic, although she reported episodes of paraesthesias with complete recovery involving the upper limbs. Electroneurographic findings were consistent with peripheral neuropathy (table 1) and the diagnosis of HNPP was established in the family. No other members were affected.

Chromosome spreads were obtained from peripheral blood of each patient and a G banding karyotype was performed. Conventional cytogenetics showed the presence of a reciprocal translocation between chromosomes 16 and 17 (t(16;17)(q12;p11.2)). FISH analysis was performed as described elsewhere using YAC 181g9 (CEPH) and cosmids c49-E4 (GDB 437232) and c103-B11 (GDB 437233) (both cosmids kindly provided by Dr P I Patel) as probes. FISH analysis showed that YAC 181g9, which encompasses marker D17S122 to marker D17S879 and contains PMP22, crossed the translocation breakpoint. FISH with cosmids c49-E4 and c103-B11 showed that the breakpoint was within cosmid c49-E4, which contains the genomic region encoding the first three exons of the PMP22 gene (fig 1). Therefore, we concluded that the PMP22 gene is interrupted in these two patients with the HNPP phenotype.

This is the first case of HNPP being caused by a reciprocal translocation that interrupts the PMP22 gene. Cytogenetic studies and FISH confirmed the diagnosis in the patient. The two cases presented here not only confirm that the HNPP phenotype was the result of the interruption of the PMP22 gene, but also show the variable penetrance of the phenotype in two related patients carrying the same mutation. It is therefore unlikely that other genes within the commonly deleted region have contributed to the phenotype. This suggests that modifiers in other genomic regions are involved in the clinical variability of peripheral neuropathies.

Table 1 Electroneurographic findings in two patients with hereditary neuropathy with liability to pressure palsies (HNPP)

<table>
<thead>
<tr>
<th>Motor and sensory nerve conduction</th>
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<th>Peroneal nerve</th>
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<td>P</td>
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<tr>
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<tr>
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<td>40</td>
<td>40</td>
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<tr>
<td>L</td>
<td>39</td>
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<tr>
<td>DL (m/sec)</td>
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<tr>
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<td>3.5</td>
<td>2.8</td>
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<tr>
<td>L</td>
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<td>3</td>
<td>3.7</td>
</tr>
<tr>
<td>(&gt;52)</td>
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<tr>
<td>SCV (m/sec)</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>R</td>
<td>35</td>
<td>43</td>
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</tr>
<tr>
<td>L</td>
<td>38</td>
<td>37</td>
<td>37</td>
</tr>
<tr>
<td>(&gt;52)</td>
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<tr>
<td>SAP amplitude (µV)</td>
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</tr>
<tr>
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<td>2</td>
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</tr>
<tr>
<td>L</td>
<td>3</td>
<td>3</td>
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</table>

P, proband; M, mother; R, right; L, left; N, normal value; MCV, motor conduction velocity; DL, distal latency; SCV, sensory conduction velocity; SAP, sensory action potential; —, not done.

The authors would like to thank Dr P I Patel for providing cosmids c49-E4 and c103-B11. This work was supported in part by Servei Català de la Salut and the Generalitat de Catalunya/CITRT/1997/SGR/00083 grant.

MARGA NADAL*†
ALBERTO VALIENTE†
ANNA DOMENECH*†
MELANIE PRITCHARD‡‡
XAVIER ESTIVILL*†
MARIA ANTONIA RAMOS-ARROYO†

*Centre de Genètica Molecular i Molecular-IBO, Institut de Recerca Oncològica, L’Hospital de Llobregat, Avenida Castellidelfis km 2, 2, 08907 Barcelona, Spain
†Servicio de Genética, Hospital Virgen del Camino, Pamplona, Spain
‡Present address: Centre for Functional Genomics and Human Disease, Monash University Medical School, Clayton, Victoria, Australia

Correspondence to: Dr Estivill, estivill@iibo.es
Figure 1  Hereditary neuropathy with liability to pressure palsies (HNPP) resulting from a t(16;17)(q12;p11.2) reciprocal translocation. (A) FISH with cosmid c103-B11 shows signals on chromosomes 17p11.2 and der(16) and does not cross the breakpoint. (B) FISH with cosmid c49-E4 (green) shows signals on chromosomes 17p11.2, der(16), and der(17), indicating that this cosmid crosses the breakpoint and that the PMP22 gene is interrupted by the reciprocal translocation. Probe D16Z1 (red) hybridises to the centromeric region of both chromosome 16 and der(16). (C) Schematic representation of the genomic region encompassing the PMP22 gene, indicating the t(16;17)(q12;p11.2) breakpoint (arrow).
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Silver-Russell syndrome and ring chromosome 7

EMMA L WAKELING, MEGAN HITCHINS, PHILIP STANIER, DAVID MONK, GUDRUN E MOORE and MICHAEL A PREECE

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